



741179.ST25.txt  
SEQUENCE LISTING

<110> Wang, Jin-Town  
Lin, Tzu-Lung

<120> A TYPE II RESTRICTION ENDONUCLEASE AND APPLICATION THEREOF

<130> P/741-179

<140> 10/796,669

<141> 2004-03-09

<160> 5

<170> PatentIn version 3.2

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<212> DNA

<213> Helicobacter pylori

<400> 1

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<212> DNA

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<221> CDS

<222> (1)..(1617)

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1 5 10 15

48

cga aac cct aaa aga ata gga caa ttt tta gct gtt tta gga aag ttt  
Arg Asn Pro Lys Arg Ile Gly Gln Phe Leu Ala Val Leu Gly Lys Phe  
20 25 30

96

gaa aat caa atc ctt aaa tct tca ata atc atg caa att atc aaa tcc  
Glu Asn Gln Ile Leu Lys Ser Ser Ile Ile Met Gln Ile Ile Lys Ser  
35 40 45

144

gtt ttg gct cat agg ctt tat aga cct act tct ctc aat caa aat aaa  
Val Leu Ala His Arg Leu Tyr Arg Pro Thr Ser Leu Asn Gln Asn Lys  
50 55 60

192

gaa ttg aaa gaa aaa ttt gac tcc aat gaa tat gtc ttt agc gat gaa  
Glu Leu Lys Glu Lys Phe Asp Ser Asn Glu Tyr Val Phe Ser Asp Glu  
65 70 75 80

240

gag tta gaa cgc att ata gaa ata tcc cca caa aat cat aaa gaa atg  
Glu Leu Glu Arg Ile Ile Glu Ile Ser Pro Gln Asn His Lys Glu Met  
85 90 95

288

ggc ttt gag cat gga tgg gaa agc cgg ttt gac act tgg tat aag ctt  
Gly Phe Glu His Gly Trp Glu Ser Arg Phe Asp Thr Trp Tyr Lys Leu  
100 105 110

336

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atg tgt gag ttt ggt ttt tgc tac tat gca aaa tat gag aaa ata ctc Met Cys Glu Phe Gly Phe Cys Tyr Tyr Ala Lys Tyr Glu Lys Ile Leu 115 120 125	384
atc agc gat agc gct aag atg ctt att ctt gct tat tac aat aaa gaa Ile Ser Asp Ser Ala Lys Met Leu Ile Leu Ala Tyr Tyr Asn Lys Glu 130 135 140	432
aac gat gct ttt aaa gaa agc gtt gat gaa agc gta gtt ggg gct ata Asn Asp Ala Phe Lys Glu Ser Val Asp Glu Ser Val Val Gly Ala Ile 145 150 155 160	480
ttt tta aac gct ctg tct aaa tat gaa gta gga aac cct tac aaa aag Phe Leu Asn Ala Leu Ser Lys Tyr Glu Val Gly Asn Pro Tyr Lys Lys 165 170 175	528
aat tta aac cat aac aac cct ttc aaa cta ttg ctc tcg ctt tta aaa Asn Leu Asn His Asn Asn Pro Phe Lys Leu Leu Leu Ser Leu Leu Lys 180 185 190	576
cga ctc aaa aat gcc cat cta acc ccc cta tct gtc aaa gaa atc cct Arg Leu Lys Asn Ala His Leu Thr Pro Leu Ser Val Lys Glu Ile Pro 195 200 205	624
att tta ctt tgt tgg aaa gac gat aac gct aat ggg ctt tat gac tac Ile Leu Cys Trp Lys Asp Asn Ala Asn Gly Leu Tyr Asp Tyr 210 215 220	672
att att cgt tta aga caa gaa atc gtt act atc aat aaa aca gaa ttc Ile Ile Arg Leu Arg Gln Glu Ile Val Thr Ile Asn Lys Thr Glu Phe 225 230 235 240	720
agc tac tca gat gaa ttt atc tat gaa aaa tgc cta aaa ctt tta gaa Ser Tyr Ser Asp Glu Phe Ile Tyr Glu Lys Cys Leu Lys Leu Leu Glu 245 250 255	768
agt gtt aat aaa aca cga ttt aaa atg agc caa atc act aac gaa gcc Ser Val Asn Lys Thr Arg Phe Lys Met Ser Gln Ile Thr Asn Glu Ala 260 265 270	816
gtt gat gaa tac att aga aaa atg cgt att aca gga ctt att tca ttg Val Asp Glu Tyr Ile Arg Lys Met Arg Ile Thr Gly Leu Ile Ser Leu 275 280 285	864
cgt ggt aat ggt agg ttt att gat att aat act aat gaa aat aat aaa Arg Gly Asn Gly Arg Phe Ile Asp Ile Asn Thr Asn Glu Asn Asn Lys 290 295 300	912
ata gat tac att tta caa acc cat aag gct ttt aaa ggg gat tat tta Ile Asp Tyr Ile Leu Gln Thr His Lys Ala Phe Lys Gly Asp Tyr Leu 305 310 315 320	960
aac gac act caa gct aac aaa ctc gcc ttt ttt aac tac atg gcg atc Asn Asp Thr Gln Ala Asn Lys Leu Ala Phe Phe Asn Tyr Met Ala Ile 325 330 335	1008
gtg gat agc ttt ctt gtt agt gtt act cca atc agc gct aat gag agc Val Asp Ser Phe Leu Val Ser Val Thr Pro Ile Ser Ala Asn Glu Ser 340 345 350	1056
gtt aaa tca agc aaa ttg aat gaa cta gca aac act tat act aaa gat Val Lys Ser Ser Lys Leu Asn Glu Leu Ala Asn Thr Tyr Thr Lys Asp 1104	

## 741179.ST25.txt

355	360	365	
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gat agt ttt tta aga ctc att gat aaa cct tta cgc tta gaa ttt tta Asp Ser Phe Leu Arg Leu Ile Asp Lys Pro Leu Arg Leu Glu Phe Leu 385 390 395 400			1200
agc gct att ttc ttg aaa caa cat ttt gaa aat tta agc gtg ata ccc Ser Ala Ile Phe Leu Lys Gln His Phe Glu Asn Leu Ser Val Ile Pro 405 410 415			1248
aat tat aaa agc gat gat gaa ggc ttg ccc gta tac aca gca agc ggt Asn Tyr Lys Ser Asp Asp Glu Gly Leu Pro Val Tyr Thr Ala Ser Gly 420 425 430			1296
aat aaa cct gat att gta gct atg gac aca aaa gcc caa agt tat ata Asn Lys Pro Asp Ile Val Ala Met Asp Thr Lys Ala Gln Ser Tyr Ile 435 440 445			1344
gaa gtg agc ttg att aga gac aga agt caa agt acc ttg gaa atg ata Glu Val Ser Leu Ile Arg Asp Arg Ser Gln Ser Thr Leu Glu Met Ile 450 455 460			1392
cct att gcc aga cat tta aaa gaa ttg att aaa aat agc acc gat att Pro Ile Ala Arg His Leu Lys Glu Leu Ile Lys Asn Ser Thr Asp Ile 465 470 475 480			1440
aga gaa aaa ttt agt gtt ttt gta gct cca aat atc cat gat gat gcc Arg Glu Lys Phe Ser Val Phe Val Ala Pro Asn Ile His Asp Asp Ala 485 490 495			1488
aaa gaa tat gcg gaa ttt gcc caa ttc aaa gac aat att aat ata tgt Lys Glu Tyr Ala Glu Phe Ala Gln Phe Lys Asp Asn Ile Asn Ile Cys 500 505 510			1536
tgt tat gct att aat gat ttt atc aaa aaa gta gaa aac agc ata gaa Cys Tyr Ala Ile Asn Asp Phe Ile Lys Lys Val Glu Asn Ser Ile Glu 515 520 525			1584
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 20 25 30

Glu Asn Gln Ile Leu Lys Ser Ser Ile Ile Met Gln Ile Ile Lys Ser  
 Page 3

35

40

45

Val Leu Ala His Arg Leu Tyr Arg Pro Thr Ser Leu Asn Gln Asn Lys  
 50 55 60

Glu Leu Lys Glu Lys Phe Asp Ser Asn Glu Tyr Val Phe Ser Asp Glu  
 65 70 75 80

Glu Leu Glu Arg Ile Ile Glu Ile Ser Pro Gln Asn His Lys Glu Met  
 85 90 95

Gly Phe Glu His Gly Trp Glu Ser Arg Phe Asp Thr Trp Tyr Lys Leu  
 100 105 110

Met Cys Glu Phe Gly Phe Cys Tyr Tyr Ala Lys Tyr Glu Lys Ile Leu  
 115 120 125

Ile Ser Asp Ser Ala Lys Met Leu Ile Leu Ala Tyr Tyr Asn Lys Glu  
 130 135 140

Asn Asp Ala Phe Lys Glu Ser Val Asp Glu Ser Val Val Gly Ala Ile  
 145 150 155 160

Phe Leu Asn Ala Leu Ser Lys Tyr Glu Val Gly Asn Pro Tyr Lys Lys  
 165 170 175

Asn Leu Asn His Asn Asn Pro Phe Lys Leu Leu Leu Ser Leu Leu Lys  
 180 185 190

Arg Leu Lys Asn Ala His Leu Thr Pro Leu Ser Val Lys Glu Ile Pro  
 195 200 205

Ile Leu Leu Cys Trp Lys Asp Asp Asn Ala Asn Gly Leu Tyr Asp Tyr  
 210 215 220

Ile Ile Arg Leu Arg Gln Glu Ile Val Thr Ile Asn Lys Thr Glu Phe  
 225 230 235 240

Ser Tyr Ser Asp Glu Phe Ile Tyr Glu Lys Cys Leu Lys Leu Leu Glu  
 245 250 255

Ser Val Asn Lys Thr Arg Phe Lys Met Ser Gln Ile Thr Asn Glu Ala  
 260 265 270

Val Asp Glu Tyr Ile Arg Lys Met Arg Ile Thr Gly Leu Ile Ser Leu  
 275 280 285

## 741179.ST25.txt

Arg Gly Asn Gly Arg Phe Ile Asp Ile Asn Thr Asn Glu Asn Asn Lys  
 290 295 300  
 Ile Asp Tyr Ile Leu Gln Thr His Lys Ala Phe Lys Gly Asp Tyr Leu  
 305 310 315 320  
 Asn Asp Thr Gln Ala Asn Lys Leu Ala Phe Phe Asn Tyr Met Ala Ile  
 325 330 335  
 Val Asp Ser Phe Leu Val Ser Val Thr Pro Ile Ser Ala Asn Glu Ser  
 340 345 350  
 Val Lys Ser Ser Lys Leu Asn Glu Leu Ala Asn Thr Tyr Thr Lys Asp  
 355 360 365  
 Phe Ile Lys Gln Glu Leu Leu Ile Thr Cys Asn Lys Gln Glu Ser Lys  
 370 375 380  
 Asp Ser Phe Leu Arg Leu Ile Asp Lys Pro Leu Arg Leu Glu Phe Leu  
 385 390 395 400  
 Ser Ala Ile Phe Leu Lys Gln His Phe Glu Asn Leu Ser Val Ile Pro  
 405 410 415  
 Asn Tyr Lys Ser Asp Asp Glu Gly Leu Pro Val Tyr Thr Ala Ser Gly  
 420 425 430  
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 435 440 445  
 Glu Val Ser Leu Ile Arg Asp Arg Ser Gln Ser Thr Leu Glu Met Ile  
 450 455 460  
 Pro Ile Ala Arg His Leu Lys Glu Leu Ile Lys Asn Ser Thr Asp Ile  
 465 470 475 480  
 Arg Glu Lys Phe Ser Val Phe Val Ala Pro Asn Ile His Asp Asp Ala  
 485 490 495  
 Lys Glu Tyr Ala Glu Phe Ala Gln Phe Lys Asp Asn Ile Asn Ile Cys  
 500 505 510  
 Cys Tyr Ala Ile Asn Asp Phe Ile Lys Lys Val Glu Asn Ser Ile Glu  
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## 741179.ST25.txt

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 ttt aat caa gct tta aag cta gaa gaa aat tat ttt agc caa cat ttt 96  
 Phe Asn Gln Ala Leu Lys Leu Glu Glu Asn Tyr Phe Ser Gln His Phe  
 20 25 30  
 agc aac aag ttt ttc agc tat aaa gat tgt gtc aaa atc ggt agc att 144  
 Ser Asn Lys Phe Phe Ser Tyr Lys Asp Cys Val Lys Ile Gly Ser Ile  
 35 40 45  
 aga gag cat ata gaa agc tta aac tta gat aaa tta aat aaa gat att 192  
 Arg Glu His Ile Glu Ser Leu Asn Leu Asp Lys Leu Asn Lys Asp Ile  
 50 55 60  
 tta tta aca agc ctg att tat tca atg gat aag ata gct aac acg gta 240  
 Leu Leu Thr Ser Leu Ile Tyr Ser Met Asp Lys Ile Ala Asn Thr Val  
 65 70 75 80  
 ggg cat tat gaa gct tat agg aaa aaa gag att ttg caa gat aga ttt 288  
 Gly His Tyr Glu Ala Tyr Arg Lys Lys Glu Ile Leu Gln Asp Arg Phe  
 85 90 95  
 att ttt gag ctt att agc cct ata aaa cat gat aaa aat atc atg ata 336  
 Ile Phe Glu Leu Ile Ser Pro Ile Lys His Asp Lys Asn Ile Met Ile  
 100 105 110  
 gag aga aaa aac gct aac gaa ttg gct aaa acc tta aaa ata gac tta 384  
 Glu Arg Lys Asn Ala Asn Glu Leu Ala Lys Thr Leu Lys Ile Asp Leu  
 115 120 125  
 gtc ttt att gat cct cca tac aat tca agg caa tac agc cgg ttt tat 432  
 Val Phe Ile Asp Pro Pro Tyr Asn Ser Arg Gln Tyr Ser Arg Phe Tyr  
 130 135 140  
 cat ctc tat gaa aac cta gtg cag tgg aaa aaa ccc aaa ctc tat gga 480  
 His Leu Tyr Glu Asn Leu Val Gln Trp Lys Lys Pro Lys Leu Tyr Gly  
 145 150 155 160  
 aca gct tta aag cca tca tgc gag aac atg agc gaa tat tgc cgc tct 528  
 Thr Ala Leu Lys Pro Ser Cys Glu Asn Met Ser Glu Tyr Cys Arg Ser  
 165 170 175  
 aat gcc aag aaa gaa ttg agc gat tta att gaa aaa cta gat tgt aaa 576  
 Asn Ala Lys Lys Glu Leu Ser Asp Leu Ile Glu Lys Leu Asp Cys Lys  
 180 185 190  
 agg att gct tta act tat aat aat acc tat aac tct aag tct agc tct 624  
 Arg Ile Ala Leu Thr Tyr Asn Asn Thr Tyr Asn Ser Lys Ser Ser Ser  
 195 200 205

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tcg caa aat aaa ata ggc ttt aaa gat tta gtg gaa att ttg agt caa	672
Ser Gln Asn Lys Ile Gly Phe Lys Asp Leu Val Glu Ile Leu Ser Gln	
210 215 220	
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Lys Gly Lys Leu Ser Val Lys Glu Lys Ala His Ser Phe Phe Asn Ser	
225 230 235 240	
gga aaa act gat ttt aaa gag cat aaa gaa ttt tta ttt ata gtg gaa	768
Gly Lys Thr Asp Phe Lys Glu His Lys Glu Phe Leu Phe Ile Val Glu	
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gag cct ttt gtg ggt ggg ggt agc gtg ttt tta aac act aag gct aag	96
Glu Pro Phe Val Gly Gly Gly Ser Val Phe Leu Asn Thr Lys Ala Lys	
20 25 30	
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Arg Tyr Leu Ala Asn Asp Ile Asp Thr Asn Ile Ile Asn Leu His Lys	
35 40 45	
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Thr Leu Ser Lys Phe Asn Val Cys Glu Leu Phe Asp Glu Leu Ser Lys	
50 55 60	
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65 70 75 80	
cct gat gaa tta aaa aaa caa tat ata aaa act tac tac gcc aaa tac	288
Pro Asp Glu Leu Lys Lys Gln Tyr Ile Lys Thr Tyr Tyr Ala Lys Tyr	
85 90 95	
aat aaa ata gct tat gaa aaa cta agg gct gat ttt aac tcc aat caa	336
Asn Lys Ile Ala Tyr Glu Lys Leu Arg Ala Asp Phe Asn Ser Asn Gln	
100 105 110	
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Asn Asn Met Leu Tyr Leu Tyr Leu Leu Ile Tyr Gly Phe Asn His	
115 120 125	
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## 741179.ST25.txt

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ttt ctt aac cac acc act tat tta aaa gat gat tat gtt tat ttt gac Phe Leu Asn His Thr Thr Tyr Leu Lys Asp Asp Tyr Val Tyr Phe Asp 180 185 190	576
ccc cct tat tta atc tcc aat agt gaa tac aac aag tta tgg gat agc Pro Pro Tyr Leu Ile Ser Asn Ser Glu Tyr Asn Lys Leu Trp Asp Ser 195 200 205	624
gat aat gag ata gcc tta tat ggt gtt tta gat agc cta gat aaa aag Asp Asn Glu Ile Ala Leu Tyr Gly Val Leu Asp Ser Leu Asp Lys Lys 210 215 220	672
gga gtt tta ttt ggt ata act aat ctt att tat cac aag gga gag act Gly Val Leu Phe Gly Ile Thr Asn Leu Ile Tyr His Lys Gly Glu Thr 225 230 235 240	720
aat ttt att tta aaa gaa tgg gct aaa aaa tat tat att ttt aat atc Asn Phe Ile Leu Lys Glu Trp Ala Lys Lys Tyr Tyr Ile Phe Asn Ile 245 250 255	768
aaa agt aat tat atc agt tat aat gac aat act att aaa gaa gat agt Lys Ser Asn Tyr Ile Ser Tyr Asn Asp Asn Thr Ile Lys Glu Asp Ser 260 265 270	816
caa gaa atc ttt gta act aat tat agg tga Gln Glu Ile Phe Val Thr Asn Tyr Arg 275 280	846